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<120> NOVEL OXIDASE

<130> Q83855

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<151> 2003-06-05

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<150> JP 2002-060749

<151> 2003-03-07

<160> 13

<170> PatentIn version 3.1

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48

gtt tgg tta ggg ctg aat gtt ttc ctg ttt gtg gat gcc ttc ctg aaa
Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys
20 25 30

96

tat gag aag gcc gac aaa tac tac tac aca aga aaa atc ctt ggg tca
Tyr Glu Lys Ala Asp Lys Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
35 40 45

144

aca ttg gcc tgt gcc cga gcg tct gct ctc tgc ttg aat ttt aac agc
Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
50 55 60

192

acg ctg atc ctg ctt cct gtg tgt cgc aat ctg ctg tcc ttc ctg agg
Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
65 70 75 80

240

ggc acc tgc tca ttt tgc agc cgc aca ctg aga aag caa ttg gat cac
Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
85 90 95

288

aac ctc acc ttc cac aag ctg gtg gcc tat atg atc tgc cta cat aca
Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
100 105 110

336

gct att cac atc att gca cac ctg ttt aac ttt gac tgc tat agc aga		384
Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg		
115	120	125
agc cga cag gcc aca gat ggc tcc ctt gcc tcc att ctc tcc agc cta		432
Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu		
130	135	140
tct cat gat gag aaa aag ggg ggt tct tgg cta aat ccc atc cag tcc		480
Ser His Asp Glu Lys Lys Gly Ser Trp Leu Asn Pro Ile Gln Ser		
145	150	155
cga aac acg aca gtg gag tat gtg aca ttc acc agc gtt gct ggt ctc		528
Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Val Ala Gly Leu		
165	170	175
act gga gtg atc atg aca ata gcc ttg att ctc atg gta act tca gct		576
Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala		
180	185	190
act gag ttc atc cgg agg agt tat ttt gaa gtc ttc tgg tat act cac		624
Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His		
195	200	205
cac ctt ttt atc ttc tat atc ctt ggc tta ggg att cac ggc att ggt		672
His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly		
210	215	220
gga att gtc cgg ggt caa aca gag gag agc atg aat gag agt cat cct		720
Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro		
225	230	235
240		
cgc aag tgt gca gag tct ttt gag atg tgg gat gat cgt gac tcc cac		768
Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His		
245	250	255
tgt agg cgc cct aag ttt gaa ggg cat ccc cct gag tct tgg aag tgg		816
Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp		
260	265	270
atc ctt gca ccg gtc att ctt tat atc tgt gaa agg atc ctc ccg ttt		864
Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe		
275	280	285
tac cgc tcc cag cag aag gtt gtg att acc aag gtt gtt atg cac cca		912
Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro		
290	295	300
tcc aaa gtt ttg gaa ttg cag atg aac aag cgt ggc ttc agc atg gaa		960
Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu		
305	310	315
320		
gtg ggg cag tat atc ttt gtt aat tgc ccc tca atc tct ctc ctg gaa		1008
Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu		
325	330	335
tgg cat cct ttt act ttg acc tct gct cca gag gaa gat ttc ttc tcc		1056
Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser		
340	345	350

att cat atc cga gca gca ggg gac tgg aca gaa aat ctc ata agg gct Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala	355	360	365	1104
ttc gaa caa caa tat tca cca att ccc agg att gaa gtg gat ggt ccc Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro	370	375	380	1152
ttt ggc aca gcc agt gag gat gtt ttc cag tat gaa gtg gct gtg ctg Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu	385	390	395	1200
gtt gga gca gga att ggg gtc acc ccc ttt gct tct atc ttg aaa tcc Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser	405	410	415	1248
atc tgg tac aaa ttc cag tgt gca gac cac aac ctc aaa aca aaa aag Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys	420	425	430	1296
gtt ggt cat gca gca tta aac ttt gac aag gcc act gac atc gtg aca Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr	435	440	445	1344
ggc ctg aaa cag aaa acc tcc ttt ggg aga cca atg tgg gac aat gag Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu	450	455	460	1392
ttt tct aca ata gct acc tcc cac ccc aag tct gta gtg gga gtt ttc Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe	465	470	475	1440
tta tgt ggc cct cgg act ttg gca aag agc ctg cgc aaa tgc tgt cac Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His	485	490	495	1488
cga tat tcc agt ctg gat cct aga aag gtt caa ttc tac ttc aac aaa Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn Lys	500	505	510	1536
gaa aat ttt tga Glu Asn Phe 515				1548

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Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val
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Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys
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Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
35 40 45

Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
50 55 60

Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
65 70 75 80

Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
85 90 95

Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
100 105 110

Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg
115 120 125

Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu
130 135 140

Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser
145 150 155 160

Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Val Ala Gly Leu
165 170 175

Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala
180 185 190

Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His
195 200 205

His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly
210 215 220

Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro
225 230 235 240

Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His
245 250 255

Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp
260 265 270

Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe
275 280 285

Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro
290 295 300

Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu
305 310 315 320

Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu
325 330 335

Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser
340 345 350

Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala
355 360 365

Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro
370 375 380

Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu
385 390 395 400

Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
405 410 415

Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys
420 425 430

Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
435 440 445

Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
450 455 460

Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe
465 470 475 480

Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His
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Glu Asn Phe
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19

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<212> DNA
<213> Homo sapiens

<400> 13
aaaaacaaaaaaaaa agatcttattt ctact

25